

In re Application of:
Cope et al.
Application No.: 10/047,253
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Page 2

PATENT
Attorney Docket No.: CIT1510-4

Amendments to the Specification

Please replace paragraphs [0024] to [0027] on pages 6-7 of the specification with the following:

[0024] FIG. 1 shows the sequence alignment of human AMSH proteins (AMSH1, is amino acid residue 281-421 of SEQ ID NO:5; AMSH2, is amino acid residues 302-461 of SEQ ID NO: 6; AMSH, SEQ ID NO: 7) with human JAB1 (SEQ ID NO:3) and Rpn11 (SEQ ID NO:4). Conserved active site residues are boxed.

[0025] FIG. 2 shows the sequence alignment of AMSH (SEQ ID NO:7), AMSH1 is amino acid residue 281-421 of SEQ ID NO:5, and AMSH2 is amino acid residues 302-461 of SEQ ID NO: 6. The critical conserved active site residues are boxed.

[0026] FIG. 3 shows that sequence alignment of COP9 subunit 5 9CSN5/JAB1(COP9 su5 Hs, SEQ ID NO:8; COP9 su5 Dm, SEQ ID NO:9; COP9 su5 At, SEQ ID NO: 10; COP9 su5 Ce, SEQ ID NO:11) and orthologs (AF2198 ArcFu, SEQ ID NO: 12; PH0451 Pyrho, SEQ ID NO:13; TVN1035 Thevo, SEQ ID NO:14; MTH971 Metth, SEQ ID NO:15; aq 1691 Aquae, SEQ ID NO:16; RV1334 Myctu, SEQ ID NO:17; and RadC Ecoli, SEQ ID NO:18) from different eukaryotic species reveals conserved histidine, serine, and aspartate residues that are also found in a set of prokaryotic and archaebacterial proteins.

[0027] FIG. 4 shows the alignment of Rpn11 orthologs (Pad1 Dm, SEQ ID NO:19; Pad1Hs, SEQ ID NO:20; and Sks1 Dd, SEQ ID NO:21; and Pad1 Sc, SEQ ID NO:22) and CSN5/JAB 1 orthologs from different species (COP9 su5 Hs, SEQ ID NO:8; COP9 su5 Dm, SEQ ID NO:9; COP9 su5 At, SEQ ID NO:10; and COP9 su5 Ce, SEQ ID NO:11).